



RECEIVED

NOV 02 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Glaxo Wellcome PLC  
Tate, Simon N  
Grose, David T  
Hicks, Caroline A

<120> Ion Channels

<130> PG3432

<140>

<141>

<150> GB 9805793.8

<151> 1998-03-18

<160> 35

<170> PatentIn Ver. 2.1

<210> 1

<211> 5897

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (49)..(5346)

<400> 1

ggagccatac ggtgccctga tcctctgtac caggaagaca gggatgaag atg gag gag 57  
Met Glu Glu  
1

agg tac tac ccg gtg atc ttc ccg gac gag cgg aat ttc cgc ccc ttc 105  
Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe Arg Pro Phe  
5 10 15

act tcc gac tct ctg gct gcc ata aag aag cgg att gct atc caa aag 153  
Thr Ser Asp Ser Leu Ala Ala Ile Lys Lys Arg Ile Ala Ile Gln Lys  
20 25 30 35

gag agg aag aag tcc aaa gac aag gcg gca gct gag ccc cag cct cgg 201  
Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro Gln Pro Arg  
40 45 50

cct cag ctt gac cta aag gcc tcc agg aag tta cct aag ctt tat ggt 249  
Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys Leu Tyr Gly  
55 60 65

gac att ccc cct gag ctt gtt acg aaa cct ctg gag gac ctg gac ccc 297  
Asp Ile Pro Pro Glu Leu Val Thr Lys Pro Leu Glu Asp Leu Asp Pro  
70 75 80

tac tac aaa gac cat aag aca ttc atg gtg ttg aac aag aaa aga aca 345

Tyr	Tyr	Lys	Asp	His	Lys	Thr	Phe	Met	Val	Leu	Asn	Lys	Lys	Arg	Thr		
85						90					95						
att	tat	cgc	ttc	agc	gcc	aag	cgg	gcc	ttg	ttc	att	ctg	ggg	cct	ttt	393	
Ile	Tyr	Arg	Phe	Ser	Ala	Lys	Arg	Ala	Leu	Phe	Ile	Leu	Gly	Pro	Phe		
100					105				110						115		
aat	ccc	ctc	aga	agc	tta	atg	att	cgt	atc	tct	gtc	cat	tca	gtc	ttt	441	
Asn	Pro	Leu	Arg	Ser	Leu	Met	Ile	Arg	Ile	Ser	Val	His	Ser	Val	Phe		
				120					125					130			
agc	atg	ttc	atc	atc	tgc	acg	gtg	atc	atc	aac	tgt	atg	ttc	atg	gcg	489	
Ser	Met	Phe	Ile	Ile	Cys	Thr	Val	Ile	Ile	Asn	Cys	Met	Phe	Met	Ala		
			135					140					145				
aat	tct	atg	gag	aga	agt	ttc	gac	aac	gac	att	ccc	gaa	tac	gtc	ttc	537	
Asn	Ser	Met	Glu	Arg	Ser	Phe	Asp	Asn	Asp	Ile	Pro	Glu	Tyr	Val	Phe		
		150					155					160					
att	ggg	att	tat	att	tta	gaa	gct	gtg	att	aaa	ata	ttg	gca	aga	ggc	585	
Ile	Gly	Ile	Tyr	Ile	Leu	Glu	Ala	Val	Ile	Lys	Ile	Leu	Ala	Arg	Gly		
	165					170					175						
ttc	att	gtg	gat	gag	ttt	tcc	ttc	ctc	cga	gat	ccg	tgg	aac	tgg	ctg	633	
Phe	Ile	Val	Asp	Glu	Phe	Ser	Phe	Leu	Arg	Asp	Pro	Trp	Asn	Trp	Leu		
180					185					190					195		
gac	ttc	att	gtc	att	gga	aca	gcg	atc	gca	act	tgt	ttt	ccg	ggc	agc	681	
Asp	Phe	Ile	Val	Ile	Gly	Thr	Ala	Ile	Ala	Thr	Cys	Phe	Pro	Gly	Ser		
				200					205					210			
caa	gtc	aat	ctt	tca	gct	ctt	cgt	acc	ttc	cga	gtg	ttc	aga	gct	ctg	729	
Gln	Val	Asn	Leu	Ser	Ala	Leu	Arg	Thr	Phe	Arg	Val	Phe	Arg	Ala	Leu		
			215					220					225				
aag	gcg	att	tca	gtt	atc	tca	ggg	ctg	aag	gtc	atc	gta	ggg	gcc	ctg	777	
Lys	Ala	Ile	Ser	Val	Ile	Ser	Gly	Leu	Lys	Val	Ile	Val	Gly	Ala	Leu		
		230					235					240					
ctg	cgc	tcg	gtg	aag	aag	ctg	gta	gac	gtg	atg	gtc	ctc	act	ctc	ttc	825	
Leu	Arg	Ser	Val	Lys	Lys	Leu	Val	Asp	Val	Met	Val	Leu	Thr	Leu	Phe		
	245					250					255						
tgc	ctc	agc	atc	ttt	gcc	ctg	gtc	ggg	cag	cag	ctg	ttc	atg	gga	att	873	
Cys	Leu	Ser	Ile	Phe	Ala	Leu	Val	Gly	Gln	Gln	Leu	Phe	Met	Gly	Ile		
	260				265					270					275		
ctg	aac	cag	aag	tgt	att	aag	cac	aac	tgt	ggc	ccc	aac	cct	gca	tcc	921	
Leu	Asn	Gln	Lys	Cys	Ile	Lys	His	Asn	Cys	Gly	Pro	Asn	Pro	Ala	Ser		
				280					285					290			
aac	aag	gat	tgc	ttt	gaa	aag	gaa	aaa	gat	agc	gaa	gac	ttc	ata	atg	969	
Asn	Lys	Asp	Cys	Phe	Glu	Lys	Glu	Lys	Asp	Ser	Glu	Asp	Phe	Ile	Met		
			295					300					305				
tgt	ggg	acc	tgg	ctc	ggc	agc	aga	ccc	tgt	ccc	aat	ggg	tct	acg	tgc	1017	
Cys	Gly	Thr	Trp	Leu	Gly	Ser	Arg	Pro	Cys	Pro	Asn	Gly	Ser	Thr	Cys		

C'  
cont.

310	315	320	
gat aaa acc aca ttg aac cca gac aat aat tat aca aag ttt gac aac Asp Lys Thr Thr Leu Asn Pro Asp Asn Asn Tyr Thr Lys Phe Asp Asn 325 330 335			1065
ttt ggc tgg tcc ttt ctc gcc atg ttc cgg gtt atg act caa gac tcc Phe Gly Trp Ser Phe Leu Ala Met Phe Arg Val Met Thr Gln Asp Ser 340 345 350 355			1113
tgg gag agg ctt tac cga cag atc ctg cgg acc tct ggg atc tac ttt Trp Glu Arg Leu Tyr Arg Gln Ile Leu Arg Thr Ser Gly Ile Tyr Phe 360 365 370			1161
gtc ttc ttc ttc gtg gtg gtc atc ttc ctg ggc tcc ttc tac ctg ctt Val Phe Phe Phe Val Val Val Ile Phe Leu Gly Ser Phe Tyr Leu Leu 375 380 385			1209
aac cta acc ctg gct gtt gtc acc atg gct tat gaa gaa cag aac aga Asn Leu Thr Leu Ala Val Val Thr Met Ala Tyr Glu Glu Gln Asn Arg 390 395 400			1257
aat gta gct gct gag aca gag gcc aag gag aaa atg ttt cag gaa gcc Asn Val Ala Ala Glu Thr Glu Ala Lys Glu Lys Met Phe Gln Glu Ala 405 410 415			1305
cag cag ctg tta agg gag gag aag gag gct ctg gtt gcc atg gga att Gln Gln Leu Leu Arg Glu Glu Lys Glu Ala Leu Val Ala Met Gly Ile 420 425 430 435			1353
gac aga agt tcc ctt aat tcc ctt caa gct tca tcc ttt tcc ccg aag Asp Arg Ser Ser Leu Asn Ser Leu Gln Ala Ser Ser Phe Ser Pro Lys 440 445 450			1401
aag agg aag ttt ttc ggt agt aag aca aga aag tcc ttc ttt atg aga Lys Arg Lys Phe Phe Gly Ser Lys Thr Arg Lys Ser Phe Phe Met Arg 455 460 465			1449
ggg tcc aag acg gcc caa gcc tca gcg tct gat tca gag gac gat gcc Gly Ser Lys Thr Ala Gln Ala Ser Ala Ser Asp Ser Glu Asp Asp Ala 470 475 480			1497
tct aaa aat cca cag ctc ctt gag cag acc aaa cga ctg tcc cag aac Ser Lys Asn Pro Gln Leu Leu Glu Gln Thr Lys Arg Leu Ser Gln Asn 485 490 495			1545
ttg cca gtg gat ctc ttt gat gag cac gtg gac ccc ctc cac agg cag Leu Pro Val Asp Leu Phe Asp Glu His Val Asp Pro Leu His Arg Gln 500 505 510 515			1593
aga gcg ctg agc gct gtc agt atc tta acc atc acc ata cag gaa caa Arg Ala Leu Ser Ala Val Ser Ile Leu Thr Ile Thr Ile Gln Glu Gln 520 525 530			1641
gaa aaa ttc cag gag cct tgt ttc cca tgt ggg aaa aat ttg gcc tct Glu Lys Phe Gln Glu Pro Cys Phe Pro Cys Gly Lys Asn Leu Ala Ser 535 540 545			1689

C'  
cont

aag tac ctg gtg tgg gac tgt agc cct cag tgg ctg tgc ata aag aag 1737  
Lys Tyr Leu Val Trp Asp Cys Ser Pro Gln Trp Leu Cys Ile Lys Lys  
550 555 560

gtc ctg cgg acc atc atg acg gat ccc ttt act gag ctg gcc atc acc 1785  
Val Leu Arg Thr Ile Met Thr Asp Pro Phe Thr Glu Leu Ala Ile Thr  
565 570 575

atc tgc atc atc atc aat acc gtt ttc tta gcc gtg gag cac cac aac 1833  
Ile Cys Ile Ile Ile Asn Thr Val Phe Leu Ala Val Glu His His Asn  
580 585 590 595

atg gat gac aac tta aag acc ata ctg aaa ata gga aac tgg gtt ttc 1881  
Met Asp Asp Asn Leu Lys Thr Ile Leu Lys Ile Gly Asn Trp Val Phe  
600 605 610

acg gga att ttc ata gcg gaa atg tgt ctc aag atc atc gcg ctc gac 1929  
Thr Gly Ile Phe Ile Ala Glu Met Cys Leu Lys Ile Ile Ala Leu Asp  
615 620 625

cct tac cac tac ttc cgg cac ggc tgg aat gtt ttt gac agc atc gtg 1977  
Pro Tyr His Tyr Phe Arg His Gly Trp Asn Val Phe Asp Ser Ile Val  
630 635 640

gcc ctc ctg agt ctc gct gat gtg ctc tac aac aca ctg tct gat aac 2025  
Ala Leu Leu Ser Leu Ala Asp Val Leu Tyr Asn Thr Leu Ser Asp Asn  
645 650 655

aat agg tct ttc ttg gct tcc ctc aga gtg ctg agg gtc ttc aag tta 2073  
Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val Phe Lys Leu  
660 665 670 675

gcc aaa tcc tgg ccc acg tta aac act ctc att aag atc atc ggc cac 2121  
Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly His  
680 685 690

tcc gtg ggc gcg ctt gga aac ctg act gtg gtc ctg act atc gtg gtc 2169  
Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr Ile Val Val  
695 700 705

ttc atc ttt tct gtg gtg ggc atg cgg ctc ttc ggc acc aag ttt aac 2217  
Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr Lys Phe Asn  
710 715 720

aag acc gcc tac gcc acc cag gag cgg ccc agg cgg cgc tgg cac atg 2265  
Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg Trp His Met  
725 730 735

gat aat ttc tac cac tcc ttc ctg gtg gtg ttc cgc atc ctc tgt ggg 2313  
Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly  
740 745 750 755

gaa tgg atc gag aac atg tgg ggc tgc atg cag gat atg gac ggc tcc 2361  
Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met Asp Gly Ser  
760 765 770

C  
cont.

ccg ttg tgc atc att gtc ttt gtc ctg ata atg gtg atc ggg aag ctt	2409
Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile Gly Lys Leu	
775 780 785	
gtg gtg ctt aac ctc ttc att gcc ttg ctg ctc aat tcc ttc agc aat	2457
Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Asn	
790 795 800	
gag gag aag gat ggg agc ctg gaa gga gag acc agg aaa acc aaa gtg	2505
Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys Thr Lys Val	
805 810 815	
cag cta gcc ctg gat cgg ttc cgc cgg gcc ttc tcc ttc atg ctg cac	2553
Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe Met Leu His	
820 825 830 835	
gct ctt cag agt ttt tgt tgc aag aaa tgc agg agg aaa aac tcg cca	2601
Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys Asn Ser Pro	
840 845 850	
aag cca aaa gag aca aca gaa agc ttt gct ggt gag aat aaa gac tca	2649
Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn Lys Asp Ser	
855 860 865	
atc ctc ccg gat gcg agg ccc tgg aag gag tat gat aca gac atg gct	2697
Ile Leu Pro Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr Asp Met Ala	
870 875 880	
ttg tac act gga cag gcc ggg gct ccg ctg gcc cca ctc gca gag gta	2745
Leu Tyr Thr Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu Ala Glu Val	
885 890 895	
gag gac gat gtg gaa tat tgt ggt gaa ggc ggt gcc cta ccc acc tca	2793
Glu Asp Asp Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu Pro Thr Ser	
900 905 910 915	
caa cat agt gct gga gtt cag gcc ggt gac ctc cct cca gag acc aag	2841
Gln His Ser Ala Gly Val Gln Ala Gly Asp Leu Pro Pro Glu Thr Lys	
920 925 930	
cag ctc act agc ccg gat gac caa ggg gtt gaa atg gaa gta ttt tct	2889
Gln Leu Thr Ser Pro Asp Asp Gln Gly Val Glu Met Glu Val Phe Ser	
935 940 945	
gaa gaa gat ctg cat tta agc ata cag agt cct cga aag aag tct gac	2937
Glu Glu Asp Leu His Leu Ser Ile Gln Ser Pro Arg Lys Lys Ser Asp	
950 955 960	
gca gtg agc atg ctc tcg gaa tgc agc aca att gac ctg aat gat atc	2985
Ala Val Ser Met Leu Ser Glu Cys Ser Thr Ile Asp Leu Asn Asp Ile	
965 970 975	
ttt aga aat tta cag aaa aca gtt tcc ccc aaa aag cag cca gat aga	3033
Phe Arg Asn Leu Gln Lys Thr Val Ser Pro Lys Lys Gln Pro Asp Arg	
980 985 990 995	
tgc ttt ccc aag ggc ctt agt tgt cac ttt cta tgc cac aaa aca gac	3081

C1  
cont.

Cys	Phe	Pro	Lys	Gly	Leu	Ser	Cys	His	Phe	Leu	Cys	His	Lys	Thr	Asp		
				1000					1005					1010			
aag	aga	aag	tcc	ccc	tgg	gtc	ctg	tgg	tgg	aac	att	cgg	aaa	acc	tgc	3129	
Lys	Arg	Lys	Ser	Pro	Trp	Val	Leu	Trp	Trp	Asn	Ile	Arg	Lys	Thr	Cys		
			1015				1020					1025					
tac	caa	atc	gtg	aag	cac	agc	tgg	ttt	gag	agt	ttc	ata	atc	ttt	gtt	3177	
Tyr	Gln	Ile	Val	Lys	His	Ser	Trp	Phe	Glu	Ser	Phe	Ile	Ile	Phe	Val		
		1030				1035					1040						
att	ctg	ctg	agc	agt	gga	gcg	ctg	ata	ttt	gaa	gat	gtc	aat	ctc	ccc	3225	
Ile	Leu	Leu	Ser	Ser	Gly	Ala	Leu	Ile	Phe	Glu	Asp	Val	Asn	Leu	Pro		
	1045				1050					1055							
agc	cgg	ccc	caa	gtt	gag	aaa	tta	cta	agg	tgt	acc	gat	aat	att	ttc	3273	
Ser	Arg	Pro	Gln	Val	Glu	Lys	Leu	Leu	Arg	Cys	Thr	Asp	Asn	Ile	Phe		
1060				1065					1070					1075			
aca	ttt	att	ttc	ctc	ctg	gaa	atg	atc	ctg	aag	tgg	gtg	gcc	ttt	gga	3321	
Thr	Phe	Ile	Phe	Leu	Leu	Glu	Met	Ile	Leu	Lys	Trp	Val	Ala	Phe	Gly		
			1080			1085					1090						
ttc	cgg	agg	tat	ttc	acc	agt	gcc	tgg	tgc	tgg	ctt	gat	ttc	ctc	att	3369	
Phe	Arg	Arg	Tyr	Phe	Thr	Ser	Ala	Trp	Cys	Trp	Leu	Asp	Phe	Leu	Ile		
		1095				1100					1105						
gtg	gtg	gtg	tct	gtg	ctc	agt	ctc	atg	aat	cta	cca	agc	ttg	aag	tcc	3417	
Val	Val	Val	Ser	Val	Leu	Ser	Leu	Met	Asn	Leu	Pro	Ser	Leu	Lys	Ser		
		1110			1115					1120							
ttc	cgg	act	ctg	cgg	gcc	ctg	aga	cct	ctg	cgg	gcg	ctg	tcc	cag	ttt	3465	
Phe	Arg	Thr	Leu	Arg	Ala	Leu	Arg	Pro	Leu	Arg	Ala	Leu	Ser	Gln	Phe		
	1125			1130				1135									
gaa	gga	atg	aag	gtt	gtc	gtc	tac	gcc	ctg	atc	agc	gcc	ata	cct	gcc	3513	
Glu	Gly	Met	Lys	Val	Val	Val	Tyr	Ala	Leu	Ile	Ser	Ala	Ile	Pro	Ala		
1140				1145				1150					1155				
att	ctc	aat	gtc	ttg	ctg	gtc	tgc	ctc	att	ttc	tgg	ctc	gta	ttt	tgt	3561	
Ile	Leu	Asn	Val	Leu	Leu	Val	Cys	Leu	Ile	Phe	Trp	Leu	Val	Phe	Cys		
			1160			1165						1170					
atc	ttg	gga	gta	aat	tta	ttt	tct	ggg	aag	ttt	gga	agg	tgc	att	aac	3609	
Ile	Leu	Gly	Val	Asn	Leu	Phe	Ser	Gly	Lys	Phe	Gly	Arg	Cys	Ile	Asn		
		1175			1180						1185						
ggg	aca	gac	ata	aat	atg	tat	ttg	gat	ttt	acc	gaa	gtt	ccg	aac	cga	3657	
Gly	Thr	Asp	Ile	Asn	Met	Tyr	Leu	Asp	Phe	Thr	Glu	Val	Pro	Asn	Arg		
	1190			1195				1200									
agc	caa	tgt	aac	att	agt	aat	tac	tcg	tgg	aag	gtc	ccg	cag	gtc	aac	3705	
Ser	Gln	Cys	Asn	Ile	Ser	Asn	Tyr	Ser	Trp	Lys	Val	Pro	Gln	Val	Asn		
	1205			1210				1215									
ttt	gac	aac	gtg	ggg	aat	gcc	tat	ctc	gcc	ctg	ctg	caa	gtg	gca	acc	3753	
Phe	Asp	Asn	Val	Gly	Asn	Ala	Tyr	Leu	Ala	Leu	Leu	Gln	Val	Ala	Thr		

C1  
ant.

1220	1225	1230	1235	
tat aag ggc tgg ctg gaa atc atg aat gct gct gtc gat tcc aga gag				3801
Tyr Lys Gly Trp Leu Glu Ile Met Asn Ala Ala Val Asp Ser Arg Glu				
	1240	1245	1250	
aaa gac gag cag ccg gac ttt gag gcg aac ctc tac gcg tat ctc tac				3849
Lys Asp Glu Gln Pro Asp Phe Glu Ala Asn Leu Tyr Ala Tyr Leu Tyr				
	1255	1260	1265	
ttt gtg gtt ttt atc atc ttc ggc tcc ttc ttt acc ctg aac ctc ttt				3897
Phe Val Val Phe Ile Ile Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe				
	1270	1275	1280	
atc ggt gtt att att gac aac ttc aat cag cag cag aaa aag tta ggt				3945
Ile Gly Val Ile Ile Asp Asn Phe Asn Gln Gln Gln Lys Lys Leu Gly				
	1285	1290	1295	
ggc caa gac att ttt atg aca gaa gaa cag aag aaa tat tac aat gca				3993
Gly Gln Asp Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala				
	1300	1305	1310	1315
atg aaa aag tta gga acc aag aaa cct caa aag ccc atc cca agg ccc				4041
Met Lys Lys Leu Gly Thr Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro				
	1320	1325	1330	
ctg aac aaa tgt caa gcc ttt gtg ttc gac ctg gtc aca agc cag gtc				4089
Leu Asn Lys Cys Gln Ala Phe Val Phe Asp Leu Val Thr Ser Gln Val				
	1335	1340	1345	
ttt gac gtc atc att ctg ggt ctt att gtc tta aat atg att atc atg				4137
Phe Asp Val Ile Ile Leu Gly Leu Ile Val Leu Asn Met Ile Ile Met				
	1350	1355	1360	
atg gct gaa tct gcc gac cag ccc aaa gat gtg aag aaa acc ttt gat				4185
Met Ala Glu Ser Ala Asp Gln Pro Lys Asp Val Lys Lys Thr Phe Asp				
	1365	1370	1375	
atc ctc aac ata gcc ttc gtg gtc atc ttt acc ata gag tgt ctc atc				4233
Ile Leu Asn Ile Ala Phe Val Val Ile Phe Thr Ile Glu Cys Leu Ile				
	1380	1385	1390	1395
aaa gtc ttt gct ttg agg caa cac tac ttc acc aat ggc tgg aac tta				4281
Lys Val Phe Ala Leu Arg Gln His Tyr Phe Thr Asn Gly Trp Asn Leu				
	1400	1405	1410	
ttt gat tgt gtg gtc gtg gtt ctt tct atc att agt acc ctg gtt tcc				4329
Phe Asp Cys Val Val Val Val Leu Ser Ile Ile Ser Thr Leu Val Ser				
	1415	1420	1425	
cgc ttg gag gac agt gac att tct ttc ccg ccc acg ctc ttc aga gtc				4377
Arg Leu Glu Asp Ser Asp Ile Ser Phe Pro Pro Thr Leu Phe Arg Val				
	1430	1435	1440	
gtc cgc ttg gct cgg att ggt cga atc ctc agg ctg gtc cgg gct gcc				4425
Val Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Val Arg Ala Ala				
	1445	1450	1455	

C1  
cont.

cgg gga atc agg acc ctc ctc ttt gct ttg atg atg tct ctc ccc tct 4473  
 Arg Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ser  
 1460 1465 1470 1475

ctc ttc aac atc ggt ctg ctg ctc ttc ctg gtg atg ttc att tac gcc 4521  
 Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ala  
 1480 1485 1490

atc ttt ggg atg agc tgg ttt tcc aaa gtg aag aag ggc tcc ggg atc 4569  
 Ile Phe Gly Met Ser Trp Phe Ser Lys Val Lys Lys Gly Ser Gly Ile  
 1495 1500 1505

gac gac atc ttc aac ttc gag acc ttt acg ggc agc atg ctg tgc ctc 4617  
 Asp Asp Ile Phe Asn Phe Glu Thr Phe Thr Gly Ser Met Leu Cys Leu  
 1510 1515 1520

ttc cag ata acc act tcg gct ggc tgg gat acc ctc ctc aac ccc atg 4665  
 Phe Gln Ile Thr Thr Ser Ala Gly Trp Asp Thr Leu Leu Asn Pro Met  
 1525 1530 1535

ctg gag gca aaa gaa cac tgc aac tcc tcc tcc caa gac agc tgt cag 4713  
 Leu Glu Ala Lys Glu His Cys Asn Ser Ser Ser Gln Asp Ser Cys Gln  
 1540 1545 1550 1555

cag ccg cag ata gcc gtc gtc tac ttc gtc agt tac atc atc atc tcc 4761  
 Gln Pro Gln Ile Ala Val Val Tyr Phe Val Ser Tyr Ile Ile Ile Ser  
 1560 1565 1570

ttc ctc atc gtg gtc aac atg tac atc gct gtg atc ctc gag aac ttc 4809  
 Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe  
 1575 1580 1585

aac aca gcc acg gag gag agc gag gac cct ctg gga gag gac gac ttt 4857  
 Asn Thr Ala Thr Glu Glu Ser Glu Asp Pro Leu Gly Glu Asp Asp Phe  
 1590 1595 1600

gaa atc ttc tat gag gtc tgg gag aag ttt gac ccc gag gcg tcg cag 4905  
 Glu Ile Phe Tyr Glu Val Trp Glu Lys Phe Asp Pro Glu Ala Ser Gln  
 1605 1610 1615

ttc atc cag tat tcg gcc ctc tct gac ttt gcg gac gcc ctg ccg gag 4953  
 Phe Ile Gln Tyr Ser Ala Leu Ser Asp Phe Ala Asp Ala Leu Pro Glu  
 1620 1625 1630 1635

ccg ttg cgt gtg gcc aag ccg aat aag ttt cag ttt cta gtg atg gac 5001  
 Pro Leu Arg Val Ala Lys Pro Asn Lys Phe Gln Phe Leu Val Met Asp  
 1640 1645 1650

ttg ccc atg gtg atg ggc gac cgc ctc cat tgc atg gat gtt ctc ttt 5049  
 Leu Pro Met Val Met Gly Asp Arg Leu His Cys Met Asp Val Leu Phe  
 1655 1660 1665

gct ttc act acc agg gtc ctc ggg gac tcc agc ggc ttg gat acc atg 5097  
 Ala Phe Thr Thr Arg Val Leu Gly Asp Ser Ser Gly Leu Asp Thr Met  
 1670 1675 1680

C'  
 ant.

aaa acc atg atg gag gag aag ttt atg gag gcc aac cct ttt aag aag 5145  
 Lys Thr Met Met Glu Glu Lys Phe Met Glu Ala Asn Pro Phe Lys Lys  
 1685 1690 1695

ctc tac gag ccc ata gtc acc acc acc aag agg aag gag gag gag caa 5193  
 Leu Tyr Glu Pro Ile Val Thr Thr Thr Lys Arg Lys Glu Glu Glu Gln  
 1700 1705 1710 1715

ggc gcc gcc gtc atc cag agg gcc tac cgg aaa cac atg gag aag atg 5241  
 Gly Ala Ala Val Ile Gln Arg Ala Tyr Arg Lys His Met Glu Lys Met  
 1720 1725 1730

gtc aaa ctg agg ctg aag gac agg tca agt tca tcg cac cag gtg ttt 5289  
 Val Lys Leu Arg Leu Lys Asp Arg Ser Ser Ser His Gln Val Phe  
 1735 1740 1745

tgc aat gga gac ttg tcc agc ttg gat gtg gcc aag gtc aag gtt cac 5337  
 Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala Lys Val Lys Val His  
 1750 1755 1760

aat gac tga accctcatct ccacccctac ctactgcct cacagcttag 5386  
 Asn Asp  
 1765

cctccagcct ctggcgagca ggcggcagac tcaactgaaca caggccgttc gatctgtgtt 5446

tttggctgaa cgaggtgaca ggttggcgtc cttttttaaa tgactcttgg aaagatttca 5506

tgtagagaga tgttagaagg gactgcaaag gacaccgacc ataacggaag gcctggagga 5566

cagtccaact tacataaaga tgagaaacaa gaaggaaaga tcccaggaaa acttcagatt 5626

gtgttctcag tacattcccc aatgtgtctg ttcgggtgtt tgagtatgtg acctgccaca 5686

tgtagctctt ttttgcattg acgtcaaaac cctgcagtaa gttaatatgt tgctacgggt 5746

gttcctacca gcatcacaga attgggtgta tgactcaaac ctaaaagcat gactctgact 5806

tgtagctcag caccgccact ttcagacgt ccaatctctg tcccaggtgt ctaacgaata 5866

aataggtaaa agaaaaaaaa aaaaaaaaaa a 5897

<210> 2

<211> 1765

<212> PRT

<213> Rattus norvegicus

<400> 2

Met Glu Glu Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe  
 1 5 10 15

Arg Pro Phe Thr Ser Asp Ser Leu Ala Ala Ile Lys Lys Arg Ile Ala  
 20 25 30

Ile Gln Lys Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro  
 35 40 45

C' end.

Gln Pro Arg Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys  
 50 55 60  
 Leu Tyr Gly Asp Ile Pro Pro Glu Leu Val Thr Lys Pro Leu Glu Asp  
 65 70 75 80  
 Leu Asp Pro Tyr Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys  
 85 90 95  
 Lys Arg Thr Ile Tyr Arg Phe Ser Ala Lys Arg Ala Leu Phe Ile Leu  
 100 105 110  
 Gly Pro Phe Asn Pro Leu Arg Ser Leu Met Ile Arg Ile Ser Val His  
 115 120 125  
 Ser Val Phe Ser Met Phe Ile Ile Cys Thr Val Ile Ile Asn Cys Met  
 130 135 140  
 Phe Met Ala Asn Ser Met Glu Arg Ser Phe Asp Asn Asp Ile Pro Glu  
 145 150 155 160  
 Tyr Val Phe Ile Gly Ile Tyr Ile Leu Glu Ala Val Ile Lys Ile Leu  
 165 170 175  
 Ala Arg Gly Phe Ile Val Asp Glu Phe Ser Phe Leu Arg Asp Pro Trp  
 180 185 190  
 Asn Trp Leu Asp Phe Ile Val Ile Gly Thr Ala Ile Ala Thr Cys Phe  
 195 200 205  
 Pro Gly Ser Gln Val Asn Leu Ser Ala Leu Arg Thr Phe Arg Val Phe  
 210 215 220  
 Arg Ala Leu Lys Ala Ile Ser Val Ile Ser Gly Leu Lys Val Ile Val  
 225 230 235 240  
 Gly Ala Leu Leu Arg Ser Val Lys Lys Leu Val Asp Val Met Val Leu  
 245 250 255  
 Thr Leu Phe Cys Leu Ser Ile Phe Ala Leu Val Gly Gln Gln Leu Phe  
 260 265 270  
 Met Gly Ile Leu Asn Gln Lys Cys Ile Lys His Asn Cys Gly Pro Asn  
 275 280 285  
 Pro Ala Ser Asn Lys Asp Cys Phe Glu Lys Glu Lys Asp Ser Glu Asp  
 290 295 300  
 Phe Ile Met Cys Gly Thr Trp Leu Gly Ser Arg Pro Cys Pro Asn Gly  
 305 310 315 320  
 Ser Thr Cys Asp Lys Thr Thr Leu Asn Pro Asp Asn Asn Tyr Thr Lys  
 325 330 335  
 Phe Asp Asn Phe Gly Trp Ser Phe Leu Ala Met Phe Arg Val Met Thr  
 340 345 350

C1  
cont.

Gln Asp Ser Trp Glu Arg Leu Tyr Arg Gln Ile Leu Arg Thr Ser Gly  
 355 360 365  
 Ile Tyr Phe Val Phe Phe Phe Val Val Val Ile Phe Leu Gly Ser Phe  
 370 375 380  
 Tyr Leu Leu Asn Leu Thr Leu Ala Val Val Thr Met Ala Tyr Glu Glu  
 385 390 395 400  
 Gln Asn Arg Asn Val Ala Ala Glu Thr Glu Ala Lys Glu Lys Met Phe  
 405 410 415  
 Gln Glu Ala Gln Gln Leu Leu Arg Glu Glu Lys Glu Ala Leu Val Ala  
 420 425 430  
 Met Gly Ile Asp Arg Ser Ser Leu Asn Ser Leu Gln Ala Ser Ser Phe  
 435 440 445  
 Ser Pro Lys Lys Arg Lys Phe Phe Gly Ser Lys Thr Arg Lys Ser Phe  
 450 455 460  
 Phe Met Arg Gly Ser Lys Thr Ala Gln Ala Ser Ala Ser Asp Ser Glu  
 465 470 475 480  
 Asp Asp Ala Ser Lys Asn Pro Gln Leu Leu Glu Gln Thr Lys Arg Leu  
 485 490 495  
 Ser Gln Asn Leu Pro Val Asp Leu Phe Asp Glu His Val Asp Pro Leu  
 500 505 510  
 His Arg Gln Arg Ala Leu Ser Ala Val Ser Ile Leu Thr Ile Thr Ile  
 515 520 525  
 Gln Glu Gln Glu Lys Phe Gln Glu Pro Cys Phe Pro Cys Gly Lys Asn  
 530 535 540  
 Leu Ala Ser Lys Tyr Leu Val Trp Asp Cys Ser Pro Gln Trp Leu Cys  
 545 550 555 560  
 Ile Lys Lys Val Leu Arg Thr Ile Met Thr Asp Pro Phe Thr Glu Leu  
 565 570 575  
 Ala Ile Thr Ile Cys Ile Ile Ile Asn Thr Val Phe Leu Ala Val Glu  
 580 585 590  
 His His Asn Met Asp Asp Asn Leu Lys Thr Ile Leu Lys Ile Gly Asn  
 595 600 605  
 Trp Val Phe Thr Gly Ile Phe Ile Ala Glu Met Cys Leu Lys Ile Ile  
 610 615 620  
 Ala Leu Asp Pro Tyr His Tyr Phe Arg His Gly Trp Asn Val Phe Asp  
 625 630 635 640  
 Ser Ile Val Ala Leu Leu Ser Leu Ala Asp Val Leu Tyr Asn Thr Leu  
 645 650 655

C1  
cont.

Ser Asp Asn Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val  
660 665 670

Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile  
675 680 685

Ile Gly His Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr  
690 695 700

Ile Val Val Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr  
705 710 715 720

Lys Phe Asn Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg  
725 730 735

Trp His Met Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile  
740 745 750

Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met  
755 760 765

Asp Gly Ser Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile  
770 775 780

Gly Lys Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser  
785 790 795 800

Phe Ser Asn Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys  
805 810 815

Thr Lys Val Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe  
820 825 830

Met Leu His Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys  
835 840 845

Asn Ser Pro Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn  
850 855 860

Lys Asp Ser Ile Leu Pro Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr  
865 870 875 880

Asp Met Ala Leu Tyr Thr Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu  
885 890 895

Ala Glu Val Glu Asp Asp Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu  
900 905 910

Pro Thr Ser Gln His Ser Ala Gly Val Gln Ala Gly Asp Leu Pro Pro  
915 920 925

Glu Thr Lys Gln Leu Thr Ser Pro Asp Asp Gln Gly Val Glu Met Glu  
930 935 940

Val Phe Ser Glu Glu Asp Leu His Leu Ser Ile Gln Ser Pro Arg Lys  
945 950 955 960

C1  
cont.

Lys Ser Asp Ala Val Ser Met Leu Ser Glu Cys Ser Thr Ile Asp Leu  
 965 970 975  
 Asn Asp Ile Phe Arg Asn Leu Gln Lys Thr Val Ser Pro Lys Lys Gln  
 980 985 990  
 Pro Asp Arg Cys Phe Pro Lys Gly Leu Ser Cys His Phe Leu Cys His  
 995 1000 1005  
 Lys Thr Asp Lys Arg Lys Ser Pro Trp Val Leu Trp Trp Asn Ile Arg  
 1010 1015 1020  
 Lys Thr Cys Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser Phe Ile  
 1025 1030 1035 1040  
 Ile Phe Val Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe Glu Asp Val  
 1045 1050 1055  
 Asn Leu Pro Ser Arg Pro Gln Val Glu Lys Leu Leu Arg Cys Thr Asp  
 1060 1065 1070  
 Asn Ile Phe Thr Phe Ile Phe Leu Leu Glu Met Ile Leu Lys Trp Val  
 1075 1080 1085  
 Ala Phe Gly Phe Arg Arg Tyr Phe Thr Ser Ala Trp Cys Trp Leu Asp  
 1090 1095 1100  
 Phe Leu Ile Val Val Val Ser Val Leu Ser Leu Met Asn Leu Pro Ser  
 1105 1110 1115 1120  
 Leu Lys Ser Phe Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu  
 1125 1130 1135  
 Ser Gln Phe Glu Gly Met Lys Val Val Val Tyr Ala Leu Ile Ser Ala  
 1140 1145 1150  
 Ile Pro Ala Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu  
 1155 1160 1165  
 Val Phe Cys Ile Leu Gly Val Asn Leu Phe Ser Gly Lys Phe Gly Arg  
 1170 1175 1180  
 Cys Ile Asn Gly Thr Asp Ile Asn Met Tyr Leu Asp Phe Thr Glu Val  
 1185 1190 1195 1200  
 Pro Asn Arg Ser Gln Cys Asn Ile Ser Asn Tyr Ser Trp Lys Val Pro  
 1205 1210 1215  
 Gln Val Asn Phe Asp Asn Val Gly Asn Ala Tyr Leu Ala Leu Leu Gln  
 1220 1225 1230  
 Val Ala Thr Tyr Lys Gly Trp Leu Glu Ile Met Asn Ala Ala Val Asp  
 1235 1240 1245  
 Ser Arg Glu Lys Asp Glu Gln Pro Asp Phe Glu Ala Asn Leu Tyr Ala  
 1250 1255 1260

C'  
 und.

Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Ser Phe Phe Thr Leu  
1265 1270 1275 1280

Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn Gln Gln Gln Lys  
1285 1290 1295

Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr  
1300 1305 1310

Tyr Asn Ala Met Lys Lys Leu Gly Thr Lys Lys Pro Gln Lys Pro Ile  
1315 1320 1325

Pro Arg Pro Leu Asn Lys Cys Gln Ala Phe Val Phe Asp Leu Val Thr  
1330 1335 1340

Ser Gln Val Phe Asp Val Ile Ile Leu Gly Leu Ile Val Leu Asn Met  
1345 1350 1355 1360

Ile Ile Met Met Ala Glu Ser Ala Asp Gln Pro Lys Asp Val Lys Lys  
1365 1370 1375

Thr Phe Asp Ile Leu Asn Ile Ala Phe Val Val Ile Phe Thr Ile Glu  
1380 1385 1390

Cys Leu Ile Lys Val Phe Ala Leu Arg Gln His Tyr Phe Thr Asn Gly  
1395 1400 1405

Trp Asn Leu Phe Asp Cys Val Val Val Val Leu Ser Ile Ile Ser Thr  
1410 1415 1420

Leu Val Ser Arg Leu Glu Asp Ser Asp Ile Ser Phe Pro Pro Thr Leu  
1425 1430 1435 1440

Phe Arg Val Val Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Val  
1445 1450 1455

Arg Ala Ala Arg Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser  
1460 1465 1470

Leu Pro Ser Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe  
1475 1480 1485

Ile Tyr Ala Ile Phe Gly Met Ser Trp Phe Ser Lys Val Lys Lys Gly  
1490 1495 1500

Ser Gly Ile Asp Asp Ile Phe Asn Phe Glu Thr Phe Thr Gly Ser Met  
1505 1510 1515 1520

Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly Trp Asp Thr Leu Leu  
1525 1530 1535

Asn Pro Met Leu Glu Ala Lys Glu His Cys Asn Ser Ser Ser Gln Asp  
1540 1545 1550

Ser Cys Gln Gln Pro Gln Ile Ala Val Val Tyr Phe Val Ser Tyr Ile  
1555 1560 1565

Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu  
1570 1575 1580

Glu Asn Phe Asn Thr Ala Thr Glu Glu Ser Glu Asp Pro Leu Gly Glu  
1585 1590 1595 1600

Asp Asp Phe Glu Ile Phe Tyr Glu Val Trp Glu Lys Phe Asp Pro Glu  
1605 1610 1615

Ala Ser Gln Phe Ile Gln Tyr Ser Ala Leu Ser Asp Phe Ala Asp Ala  
1620 1625 1630

Leu Pro Glu Pro Leu Arg Val Ala Lys Pro Asn Lys Phe Gln Phe Leu  
1635 1640 1645

Val Met Asp Leu Pro Met Val Met Gly Asp Arg Leu His Cys Met Asp  
1650 1655 1660

Val Leu Phe Ala Phe Thr Thr Arg Val Leu Gly Asp Ser Ser Gly Leu  
1665 1670 1675 1680

Asp Thr Met Lys Thr Met Met Glu Glu Lys Phe Met Glu Ala Asn Pro  
1685 1690 1695

Phe Lys Lys Leu Tyr Glu Pro Ile Val Thr Thr Thr Lys Arg Lys Glu  
1700 1705 1710

Glu Glu Gln Gly Ala Ala Val Ile Gln Arg Ala Tyr Arg Lys His Met  
1715 1720 1725

Glu Lys Met Val Lys Leu Arg Leu Lys Asp Arg Ser Ser Ser Ser His  
1730 1735 1740

Gln Val Phe Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala Lys Val  
1745 1750 1755 1760

Lys Val His Asn Asp  
1765

<210> 3

<211> 299

<212> DNA

<213> Homo sapiens

<400> 3

atcctagggc aggctgtttt attcccgctt cctgaggcct ttctgaggat ctgtggcttg 60

tctctgtcct gagggtgaag atggatgaca gatgctaccc agtaatcttt ccagatgagc 120

ggaatttccg ccccttcact tccgactctc tggctgcaat tgagaagcgg attgccatcc 180

aaaaggagaa aaagaagtct aaagaccaga caggagaagt accccagcct caacctcagc 240

ttgacctaaa ggctccagg aagttgccca actctatggc gacaatctc ggaggcttt 299

<210> 4  
<211> 140  
<212> DNA  
<213> Homo sapiens

<400> 4  
cgctctgtga agaagctggt caacgtgatt atcctcacct tcttttgcct cagcatcttt 60  
gccctggttag gtcagcagct cttcatggga agtctgaacc tgaaatgcat ctcgagggac 120  
tgtaaaaata tcagtaaccc 140

<210> 5  
<211> 232  
<212> DNA  
<213> Homo sapiens

<400> 5  
taaaaatatt agtaaccggg aagcttatga ccattgcttt gaaaagaaag aaaattcacc 60  
tgaattcaaa atgtgtggca tctggatggg taacagtgcc tgttcatac aatatgaatg 120  
taagcacacc aaaattaatc ctgactataa ttatacgaat ttgacaact ttggctgggc 180  
ttttcttgcc atgttcgggc tgatgaccca agattcctgg gagaagcttt at 232

C1  
only.  
<210> 6  
<211> 180  
<212> DNA  
<213> Homo sapiens

<400> 6  
actactgggt ctactcagtc ttcttcttca ttgtgggtcat tttcctgggg ctcccttcta 60  
cctgattaac ttaaaccctg gctgttggtta ccatgggcat atgaggagcc gaacaagaat 120  
gtagctgcag agatagaggc ccaggaaaag atgttcagga agcccagcag ctggttaaag 180

<210> 7  
<211> 180  
<212> DNA  
<213> Homo sapiens

<400> 7  
tatcactgga ccactttgat gagcatggag atcctctcca aaggcagaga gcactgagtg 60  
ttgtcagcat cctcaccatc accatgaagg gtaagttcca catcccaatc caagggaaag 120  
tctacttcag tgatgtcctt ccattcttct tcttcccaat ccctagaag ccctctgcaa 180

<210> 8  
<211> 299

<212> DNA  
<213> Homo sapiens

<400> 8  
gagaaatctg gattgcctca gagctaattc ctcaacctct cgcgcattct cctccagaac 60  
aagaaaaatc acaagagcct tgtctccctt gtggagaaaa cctggcatcc aagtacctcg 120  
tgtggaactg ttgccccag tggctgtgcg taaagaaggt cctgagaacc gtcattgacg 180  
tcccgtttac tgagctggac atcacgatct gcatcatcat caacacagac ttcttggaca 240  
tgagagcatca caagatgtaa ggcaacgtat tggagacgat gttgaatata gggcagtag 299

<210> 9  
<211> 335  
<212> DNA  
<213> Homo sapiens

<400> 9  
gcagatggag ttcgcttaac tggcttttct ccgttttcgt tcgtcgtttt ttctacagct 60  
caggtcttca agtaccaaat cctggccaac tttgaacaca ctaattaaga taatccggca 120  
actctcgtcg gagcccttgg aagcctgact gtggctcctg tcattgtgat ctttattttc 180  
tcagtagttg gcatgcagct ttttggccgt agcttcaatt cccaaaagag tccaaaactc 240  
tgtaaccgga caggcccgac agtctcatgt ttacggcact ggcacatggg ggatttcttg 300  
cactccttcc tagtggtatc gcgcacctc ttgcg 335

<210> 10  
<211> 261  
<212> DNA  
<213> Homo sapiens

<400> 10  
ctctgtacca aagaccctgg gcgtcaggca tgattggact tggttggcac cacttgcgga 60  
ggaggaagat gacgttgaat tttctggtga agataatgca cagcgcata cacaacctga 120  
gcctgaacaa caggtatgaa gggtcacaca tagacttaaa ggtcatacaa agctggagtt 180  
atcacagggc actggtagcc tacccttttc taggcactat gcaaggataa taaggattct 240  
cgtacgcacg ggtacgattc g 261

<210> 11  
<211> 215  
<212> DNA  
<213> Homo sapiens

<400> 11  
cagacaatga gaaactccgt actactatgg tgaaagaagg tcttagtaaa aggcaccccc 60  
ttccttttgt tctgatgtgc agaagtctga tgttaccagt atactatcag aatgtagcac 120  
cattgatctt caggatggct ttggatgggt acctgagatg gttcccaaag aaaaatttcc 180  
agcgattttt cgtaccaacg gttacgcttc gaagg 215

<210> 12  
<211> 346  
<212> DNA  
<213> Homo sapiens

<400> 12  
ttagaattcc gaatctaacc gtcgtacgag aatcctggaa tcctctaact taatggaatt 60  
agaaccttcc ggatctacga gcaactgaggc ctctcgtgcg ctgtcccagt ttgaaggaat 120  
gaaggtacat tctgcagaag aatgggtaga agttcagtta acagagaaag gtggaaagac 180  
caacagttct ttttgggctg agatttcctt aaattgccaa gcttttctctg ggttacttac 240  
cagcctgccc agtgcttaga atttgagggg tagagaaaag cctaagatat actttctacc 300  
ctaaaagctt ctgtgacagc caagatgagc tgtagcgaag gaattc 346

C'  
cont.  
<210> 13  
<211> 223  
<212> DNA  
<213> Homo sapiens

<400> 13  
gggtgcatccc taccocatct gttatggttt tcctttgctt ttgttttcca taaggtggtg 60  
gtcaatgctc tcataggtgc catacctccc attcctgaat gttttgcttg tctgcctcat 120  
tttctggctc gtattttgta ttctgggagt atacttcctt ttcttggaag atttgggaaa 180  
tgcattcaat ggaacagact tttaggaatt tccagcgatt cct 223

<210> 14  
<211> 244  
<212> DNA  
<213> Homo sapiens

<400> 14  
atcagtatta ttcattgttt tctgcttttt ttgcaggcac aatttaaggg ctggatggat 60  
atcgtttatg cagctgttga ttccacagag gtgagtcagt gttctaccat gttcggcagt 120  
gttatggcca agtcagagat atcatgacta catggacagt ccagaactgg cgtcatagtt 180  
ccagcagctg ggggttctctg ccttggtttcc tttggaacaa aacactatga gataccactg 240

ccta

244

<210> 15  
<211> 409  
<212> DNA  
<213> Homo sapiens

<400> 15  
atccacccca ggccccgcca catgccatca ctccaagctg agctgcgaaa actgaaagac 60  
aggctcccaa caggggctat ggctgttagg aagaggctat gtagtcaatg ttgctgctaa 120  
gaaacacctt ggtcttctag ataaggtagt tagaatgctt atatttttct ccagtaattg 180  
tttttttctc ttattaaaaa aatttctaac agaaagaaca acagccagag tttgagagca 240  
attcactcgg ttacatttct tcgtagtctt tatcatcttt ggctcattct tcaactctgaa 300  
tctcttcatt ggcgttatca ttgacaactt caaccaacag cagaaaaaga taagtatctg 360  
ggttgtcttg atttggtaat tgtatctctg tcttccaaag aaggaatcc 409

<210> 16  
<211> 585  
<212> DNA  
<213> Homo sapiens

C1  
ent.  
<400> 16  
tttcccagac aatacaaggt ctctgtgtgcc catagcccag gcagtctttt cgacatcatc 60  
ataagctcat acctaaacca tgattggctt gatggcctaa atatacaacc aacccccaaag 120  
ccatggaatc catccttgac catctccaac tgggtctttg tggatcatctt tacgttagaa 180  
tgtctcatca aaatctttgc tttgaggcaa tactacttca ccaatggctg gaatttatctt 240  
gactgtgtgg tcgtgcttct ttccattggt agtaagtaaa atcagcagtc agaggggactt 300  
taagaaccag aagtaagttt gtaaattctta tcattttttg aagtttggtc aaactatcca 360  
caaagcagaa aactgggcca agtgtacttt ctgaaagaat agacaggggt actaatgcca 420  
ttctctactg ggaagttgct aggagatagg aggcggtaaa tttctgggtc cccttaactc 480  
actacacaac tgaaatagag ttcaataatc atgcagctaa tgtattcaat ggaaatagac 540  
aaaattaaaa tgactcagaa gtttttgtgg tggtagaaaa atttc 585

<210> 17  
<211> 223  
<212> DNA  
<213> Homo sapiens

<400> 17  
tgaccaaggt ggaccaaatt gacttgggaa aacgggcctc attcaccact ccagactctt 60  
tgcaatggag acttgtctag ctttggggtg gccaaagggca aggtccactg tgactgagcc 120  
ctcacctcca cgcctacctc atagcttcac agccttgcct tcagcctctg agctccaggg 180  
gtcagcagct tagtgtatca acagggagtg gattcaccaa att 223

<210> 18  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18  
cctsgtcattg ttcattctac 19

<210> 19  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 19  
ctcatargar aycttggarg gg 22

<210> 20  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 20  
agggaggtca ccggcctgaa m 21

<210> 21  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 21  
agtggatmga gamcatgtgg g 21

<210> 22  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
sequence

<400> 22  
Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala Lys Val Lys Val His  
1 5 10 15

Asn Asp

<210> 23  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
sequence

C1  
cont.  
<400> 23  
Glu Glu Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Cys  
1 5 10 15

<210> 24  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 24  
gatcgaattc aaggagaaaa tgtttcagga 30

<210> 25  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 25  
gatcgtcgac tcatttggtc tgctcaagga 30

<210> 26  
<211> 30

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 26  
gatcgaattc ggcggtgccc tacccacctc 30

<210> 27  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 27  
gatcgtcgac tcattccatt tcaaccctt 30

<210> 28  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 28  
gatcgaattc aagcacaact gtggcccaa 30

<210> 29  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 29  
gatcgtcgac tcacattatg aagtcttcgc 30

<210> 30  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 30  
agtacctctc ctccatct 18

<210> 31  
<211> 18  
<212> DNA

C1  
ent.

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 31

agtactcatc cctcatct

18

<210> 32

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 32

caccgggtag tacctctc

18

<210> 33

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 33

cacgcgctag tcactctc

18

<210> 34

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 34

gtctttggac ttcttcct

18

<210> 35

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 35

gtctggtgac tctttcct

18

C'  
waf.